

## Sequence listing

<110> SHANGHAI CANCER INSTITUTE

<120> A HUMAN TUMOR-ASSOCIATED GENE CT120 ON CHROMOSOME 17P 13.3 REGION AND PROTEIN  
ENCODED BY IT

<130> 024832pc

<150> CN 02150730.9

<151> 2002-11-27

<160> 13

<170> PatentIn version 3.1

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<212> DNA

<213> Homo sapiens

〈220〉

<221> CDS

<222> (91)..(861)

<223>

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Ala Leu Phe Phe Pro Gly Leu Phe Ala Leu Cys Thr Trp Ala Leu Arg  
10                15                20

cac tcc cag ccc gga tgg agc cgc acc gac tgc gtg atg atc agc acc 210  
His Ser Gln Pro Gly Trp Ser Arg Thr Asp Cys Val Met Ile Ser Thr  
25 30 35 40

agg ctg gtt tcc tcg gtg cac gcc gtg ctg gcc acc ggc tcg ggg atc 258  
 Arg Leu Val Ser Val His Ala Val Leu Ala Thr Gly Ser Gly Ile  
           45              50              55

gtc atc att cgc tcc tgc gac gac gtg atc acc ggc agg cac tgg ctt 306  
 Val Ile Ile Arg Ser Cys Asp Asp Val Ile Thr Gly Arg His Trp Leu  
       60             65             70  
 gcc cgg gaa tat gtg tgg ttt ctg att cca tac atg atc tat gac tcg 354

Ala Arg Glu Tyr Val Trp Phe Leu Ile Pro Tyr Met Ile Tyr Asp Ser  
 75 80 85  
 tac gcc atg tac ctc tgt gaa tgg tgc cga acc aga gac cag aac cgt  
 T A G C T C T G A G G T G C C G A A C C A G A G C C G A A C G T  
 402

Tyr Ala Met Tyr Leu Cys Glu Trp Cys Arg Thr Arg Asp Gln Asn Arg  
 90                            95                            100  
 gcg ccc tcc ctc act ctt cga aac ttc cta agt cga aac cgc ctc atg      450  
 Ala Pro Ser Leu Thr Leu Arg Asn Phe Leu Ser Arg Asn Arg Leu Met

105                    110                    115                    120  
 atc aca cat cat gcg gtc att ctc ctt gtc ctt gtg cca gtc gca cag      498  
 Ile Thr His His Ala Val Ile Leu Leu Val Leu Val Pro Val Ala Gln  
 125                    130                    135

125	130	135	
agg ctc cg <sup>g</sup> gga gac ctt gg <sup>g</sup> gac ttc ttt gtc gg <sup>c</sup> tgc atc ttc acg			546
Arg Leu Arg Gly Asp Leu Gly Asp Phe Phe Val Gly Cys Ile Phe Thr			
140	145	150	

gca gaa ctg agc act ccg ttt gtg tcg ctg ggc agg gtt ctg att cag 594  
Ala Glu Leu Ser Thr Pro Phe Val Ser Leu Gly Arg Val Leu Ile Gln

155	160	165	
cta aag cag cag cac acc ctt ctg tac aag gtg aat gga atc ctc acg			642
Leu Lys Gln Gln His Thr Leu Leu Tyr Lys Val Asn Gly Ile Leu Thr			
170	175	180	
ctg gcc acc ttc ctt tcc tgc cgg atc ctt ctc ttc ccc ttc atg tac			690
Leu Ala Thr Phe Leu Ser Cys Arg Ile Leu Leu Phe Pro Phe Met Tyr			
185	190	195	200
tgg tcc tat ggc cgc cag cag gga cta agc ctg ctc caa gta ccc ttc			738
Trp Ser Tyr Gly Arg Gln Gln Gly Leu Ser Leu Leu Gln Val Pro Phe			
205	210	215	
agc atc cca ttc tac tgc aac gtg gcc aat gcc ttc ctc gta gct cct			786
Ser Ile Pro Phe Tyr Cys Asn Val Ala Asn Ala Phe Leu Val Ala Pro			
220	225	230	
cag atc tac tgg ttc tgt ctg ctg agg aag gca gtc cgg ctc ttt			834
Gln Ile Tyr Trp Phe Cys Leu Leu Cys Arg Lys Ala Val Arg Leu Phe			
235	240	245	
gac act ccc caa gcc aaa aag gat ggc taaatgctcc tgggagtcag			881
Asp Thr Pro Gln Ala Lys Lys Asp Gly			
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Thr Asp Cys Val Met Ile Ser Thr Arg Leu Val Ser Ser Val His Ala  
35 40 45  
Val Leu Ala Thr Gly Ser Gly Ile Val Ile Ile Arg Ser Cys Asp Asp  
50 55 60  
Val Ile Thr Gly Arg His Trp Leu Ala Arg Glu Tyr Val Trp Phe Leu  
65 70 75 80  
Ile Pro Tyr Met Ile Tyr Asp Ser Tyr Ala Met Tyr Leu Cys Glu Trp  
85 90 95  
Cys Arg Thr Arg Asp Gln Asn Arg Ala Pro Ser Leu Thr Leu Arg Asn  
100 105 110  
Phe Leu Ser Arg Asn Arg Leu Met Ile Thr His His Ala Val Ile Leu

115                    120                    125  
 Leu Val Leu Val Pro Val Ala Gln Arg Leu Arg Gly Asp Leu Gly Asp  
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 Phe Phe Val Gly Cys Ile Phe Thr Ala Glu Leu Ser Thr Pro Phe Val  
 145                    150                    155                    160  
 Ser Leu Gly Arg Val Leu Ile Gln Leu Lys Gln Gln His Thr Leu Leu  
 165                    170                    175  
 Tyr Lys Val Asn Gly Ile Leu Thr Leu Ala Thr Phe Leu Ser Cys Arg  
 180                    185                    190  
 Ile Leu Leu Phe Pro Phe Met Tyr Trp Ser Tyr Gly Arg Gln Gln Gly  
 195                    200                    205  
 Leu Ser Leu Leu Gln Val Pro Phe Ser Ile Pro Phe Tyr Cys Asn Val  
 210                    215                    220  
 Ala Asn Ala Phe Leu Val Ala Pro Gln Ile Tyr Trp Phe Cys Leu Leu  
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 Gly

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25

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23

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22

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Cys Arg Lys Ala Val Arg Leu Phe Asp Thr Pro Gln Ala Lys Lys  
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20